SEQUENCE LISTING

<110> Millennium Pharmaceuticals, Inc.
Meyers, Rachel
Silos-Santiago, Inmaculada

<120> 32544, a novel human phospholipase C and uses thereof

<130> 38155-20048.00

<140> US 09/927,112
<141> 2001-08-10

<150> US 60/246,808
<151> 2000-11-08

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Phe Leu Ser Ala Asn Ile Leu Pro Val Val Glu Arg Cys Met Gly Ala
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Met Gln Glu Gly Met Gln Met Val Lys Leu Arg Gly Gly Ser Lys Gly
45 50 55 60

ctg gtc cgc ttc tac tac ctg gac gag cac cgc tcc tgc atc cgc tgg 662
Leu Val Arg Phe Tyr Tyr Leu Asp Glu His Arg Ser Cys Ile Arg Trp

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cag gag gtg agt gag ggg cgg cag tcg gag gtc ttc cag cgc tac cct      758
Gln Glu Val Ser Glu Gly Arg Gln Ser Glu Val Phe Gln Arg Tyr Pro
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gac ggc agc ttc gac ccc aac tgc tgc ttc agc atc tac cac ggc agc      806
Asp Gly Ser Phe Asp Pro Asn Cys Cys Phe Ser Ile Tyr His Gly Ser
    110                 115                 120

cac cgc gag tcg ctg gac ctg gtc tcc acc agc agc gag gtg gcg cgc      854
His Arg Glu Ser Leu Asp Leu Val Ser Thr Ser Ser Glu Val Ala Arg
125                 130                 135                 140

acc tgg gtc act ggc ctg cgc tac ctc atg gcc ggc atc agc gac gag      902
Thr Trp Val Thr Gly Leu Arg Tyr Leu Met Ala Gly Ile Ser Asp Glu
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Asp Ser Leu Ala Arg Arg Gln Arg Thr Arg Asp Gln Trp Leu Lys Gln
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acg ttt gac gag gcc gac aag aac ggg gat ggc agc ctg agc att ggc      998
Thr Phe Asp Glu Ala Asp Lys Asn Gly Asp Gly Ser Leu Ser Ile Gly
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gag gtc ctg cag ctg ctg cac aag ctc aac gtg aac ctg ccc cgg cag     1046
Glu Val Leu Gln Leu Leu His Lys Leu Asn Val Asn Leu Pro Arg Gln
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Arg Val Lys Gln Met Phe Arg Glu Ala Asp Thr Asp Asp His Gln Gly
205                 210                 215                 220

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Thr Leu Gly Phe Glu Glu Phe Cys Ala Phe Tyr Lys Met Met Ser Thr
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cgc cgg gac ctc tac ctg ctc atg ctg acc tac agc aac cac aag gac     1190
Arg Arg Asp Leu Tyr Leu Leu Met Leu Thr Tyr Ser Asn His Lys Asp
            240                 245                 250

cac ctg gat gcc gcc agc ctg cag cgc ttc ctg cag gtg gag cag aag     1238
His Leu Asp Ala Ala Ser Leu Gln Arg Phe Leu Gln Val Glu Gln Lys
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atg gcg ggt gtg acc ctc gag agc tgc cag gac atc atc gag cag ttt     1286
Met Ala Gly Val Thr Leu Glu Ser Cys Gln Asp Ile Ile Glu Gln Phe
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His His His Val His Gln Asp Met Thr Gln Pro Leu Ser His Tyr Phe
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atc acc tcg tcc cac aac acc tac ctc gtg ggt gac cag ctc atg tcc      1478
Ile Thr Ser Ser His Asn Thr Tyr Leu Val Gly Asp Gln Leu Met Ser
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cag tca cgg gtg gac atg tat gct tgg gtc ctg cag gct ggc tgc cgc      1526
Gln Ser Arg Val Asp Met Tyr Ala Trp Val Leu Gln Ala Gly Cys Arg
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tgc gtg gag gtg gac tgc tgg gat ggg ccc gac ggg gag ccc att gtg      1574
Cys Val Glu Val Asp Cys Trp Asp Gly Pro Asp Gly Glu Pro Ile Val
365                 370                 375                 380

cac cat ggc tac act ctg act tcc aag atc ctc ttc aaa gac gtc att      1622
His His Gly Tyr Thr Leu Thr Ser Lys Ile Leu Phe Lys Asp Val Ile
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gaa acc atc aac aaa tat gcc ttc atc aag aat gag tac cca gtg atc      1670
Glu Thr Ile Asn Lys Tyr Ala Phe Ile Lys Asn Glu Tyr Pro Val Ile
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ctg tcc atc gaa aac cac tgc agt gtc atc cag cag aag aaa atg gcc      1718
Leu Ser Ile Glu Asn His Cys Ser Val Ile Gln Gln Lys Lys Met Ala
        415                 420                 425

cag tat ctg act gac atc ctt ggg gac aag ctg gac ctg tca tca gtg      1766
Gln Tyr Leu Thr Asp Ile Leu Gly Asp Lys Leu Asp Leu Ser Ser Val
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agc agt gaa gat gcc acc aca ctc ccc tct cca cag atg ctc aag ggc      1814
Ser Ser Glu Asp Ala Thr Thr Leu Pro Ser Pro Gln Met Leu Lys Gly
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aag atc ctc gtg aag ggg aag aag ctc cca gcc aac atc agc gag gat      1862
Lys Ile Leu Val Lys Gly Lys Lys Leu Pro Ala Asn Ile Ser Glu Asp
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gcg gag gaa ggc gag gtg tct gat gag gac agt gct gat gag att gac      1910
Ala Glu Glu Gly Glu Val Ser Asp Glu Asp Ser Ala Asp Glu Ile Asp
            480                 485                 490

gat gac tgc aag ctc ctc aat ggg gat gca tcc acc aat cga aag cgt      1958
Asp Asp Cys Lys Leu Leu Asn Gly Asp Ala Ser Thr Asn Arg Lys Arg
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gta gaa aac act gct aag agg aaa ctg gat tcc ctc atc aaa gag tcg      2006
Val Glu Asn Thr Ala Lys Arg Lys Leu Asp Ser Leu Ile Lys Glu Ser
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tcc cca tct gga aag ctc gga cgc aag agc aag gct gaa gag gac gtg     2102
Ser Pro Ser Gly Lys Leu Gly Arg Lys Ser Lys Ala Glu Glu Asp Val
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gag tct ggg gag gat gcc ggg gcc agc aga cgc aat ggc cgc ctc gtc     2150
Glu Ser Gly Glu Asp Ala Gly Ala Ser Arg Arg Asn Gly Arg Leu Val
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gtg gga agc ttc tcc agg cgc aag aag aag ggc agc aag ctg aag aag     2198
Val Gly Ser Phe Ser Arg Arg Lys Lys Lys Gly Ser Lys Leu Lys Lys
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gcg gcc agc gtg gag gag gga gat gag ggt cag gac tcc ccg gga ggc     2246
Ala Ala Ser Val Glu Glu Gly Asp Glu Gly Gln Asp Ser Pro Gly Gly
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cag agc cga ggg gcg acc cgg cag aag aag acc atg aag ctg tcc cgg     2294
Gln Ser Arg Gly Ala Thr Arg Gln Lys Lys Thr Met Lys Leu Ser Arg
605                 610                 615                 620

gcc ctc tct gac ctg gtg aag tac acc aag tcc gtg gcc acc cac gac     2342
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ata gag atg gag gcg gcg tcc agc tgg cag gtg tcg tcc ttc agc gag     2390
Ile Glu Met Glu Ala Ala Ser Ser Trp Gln Val Ser Ser Phe Ser Glu
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acc aag gcc cac cag att ctg cag cag aag ccg gcg cag tac cta cgc     2438
Thr Lys Ala His Gln Ile Leu Gln Gln Lys Pro Ala Gln Tyr Leu Arg
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ttc aac cag cag cag ctc tcc cgc atc tac ccc tcc tcc tac cgt gtg     2486
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Asp Ser Ser Asn Tyr Asn Pro Gln Pro Phe Trp Asn Ala Gly Cys Gln
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atg gtt gcc ctg aac tac cag tca gag ggg cgg atg ctg cag ctg aac     2582
Met Val Ala Leu Asn Tyr Gln Ser Glu Gly Arg Met Leu Gln Leu Asn
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cga gcc aag ttc agc gcc aac ggt ggc tgc ggc tac gta ctc aag cct     2630
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ggg tgc atg tgc cag ggc gtg ttc aac ccc aac tcg gag gac ccc ctg     2678
Gly Cys Met Cys Gln Gly Val Phe Asn Pro Asn Ser Glu Asp Pro Leu
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Gln Leu Pro Lys Pro Arg Asp Ser Met Leu Gly Asp Arg Gly Glu Ile
765                 770                 775                 780

atc gac ccc ttt gtg gag gtg gag atc att ggg ctc cct gtg gac tgc     2822
Ile Asp Pro Phe Val Glu Val Glu Ile Ile Gly Leu Pro Val Asp Cys
                785                 790                 795

agc agg gag cag acc cgc gtg gtg gac gac aac ggg ttc aac ccc acc     2870
Ser Arg Glu Gln Thr Arg Val Val Asp Asp Asn Gly Phe Asn Pro Thr
            800                 805                 810

tgg gag gag acc ctg gtt ttc atg gtg cac atg ccg gag atc gcg ctg     2918
Trp Glu Glu Thr Leu Val Phe Met Val His Met Pro Glu Ile Ala Leu
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gtc cgc ttc ctc gtc tgg gac cac gat ccc atc ggg cgt gac ttc att     2966
Val Arg Phe Leu Val Trp Asp His Asp Pro Ile Gly Arg Asp Phe Ile
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ggc cag agg acg ctg gcc ttc agc agc atg atg cca ggc tac aga cac     3014
Gly Gln Arg Thr Leu Ala Phe Ser Ser Met Met Pro Gly Tyr Arg His
845                 850                 855                 860

gtg tac cta gaa ggg atg gaa gag gcc tcc atc ttc gtg cat gtg gct     3062
Val Tyr Leu Glu Gly Met Glu Glu Ala Ser Ile Phe Val His Val Ala
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gtc agt gac atc agc ggt aag gtc aag cag gct ctg ggc cta aaa ggc     3110
Val Ser Asp Ile Ser Gly Lys Val Lys Gln Ala Leu Gly Leu Lys Gly
            880                 885                 890

ctc ttc ctc cga ggc cca aag ccc ggc tcg ctg gac agt cat gct gct     3158
Leu Phe Leu Arg Gly Pro Lys Pro Gly Ser Leu Asp Ser His Ala Ala
        895                 900                 905

ggg cgg ccc ccg gcc cgg ccc tcc gtt agc cag cgg atc ctg cgg cgc     3206
Gly Arg Pro Pro Ala Arg Pro Ser Val Ser Gln Arg Ile Leu Arg Arg
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acg gcc agc gcc ccg acc aag agc cag aag ccg ggc cgc agg ggc ttc     3254
Thr Ala Ser Ala Pro Thr Lys Ser Gln Lys Pro Gly Arg Arg Gly Phe
925                 930                 935                 940

ccg gag ctg gtc ctg ggt aca cgg gac aca ggc tcc aag ggg gtg gca     3302
Pro Glu Leu Val Leu Gly Thr Arg Asp Thr Gly Ser Lys Gly Val Ala
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Asp Asp Val Val Pro Pro Gly Pro Gly Pro Ala Pro Glu Ala Pro Ala
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Gly Pro Gly Pro Ala Gly Met Ala Ala Thr Cys Met Lys Cys Val Val
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Gly Ser Cys Ala Gly Val Asn Thr Gly Gly Leu Gln Arg Glu Arg Pro
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ccc agc ccg ggg cct gca agc agg cag gca gcc att cgc cag cag ccc     3590
Pro Ser Pro Gly Pro Ala Ser Arg Gln Ala Ala Ile Arg Gln Gln Pro
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cgg gcc cgg gct gac tca ctg ggg gcc ccc tgc tgt ggc ctg gac cct     3638
Arg Ala Arg Ala Asp Ser Leu Gly Ala Pro Cys Cys Gly Leu Asp Pro
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His Ala Ile Pro Gly Arg Ser Arg Glu Ala Pro Lys Gly Pro Gly Ala
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tgg agg cag ggt cca ggc ggt agc ggc tcc atg tcc tcg gac tcc agc     3734
Trp Arg Gln Gly Pro Gly Gly Ser Gly Ser Met Ser Ser Asp Ser Ser
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agc cca gac agc ccg ggc atc ccc gaa agg tcc ccc cgc tgg cct gag     3782
Ser Pro Asp Ser Pro Gly Ile Pro Glu Arg Ser Pro Arg Trp Pro Glu
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ttt gct caa aag ctg gag gag atc agg agt aaa tcc ccc atg ttc tcc     3878
Phe Ala Gln Lys Leu Glu Glu Ile Arg Ser Lys Ser Pro Met Phe Ser
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gcc ggt aag ccc ctc ttg ccc tgc gtg gtc ctc ccg cac gcc cct ggc     3926
Ala Gly Lys Pro Leu Leu Pro Cys Val Val Leu Pro His Ala Pro Gly
    1150                1155                1160

atg gct ggg cct ggg tca cct gct gct gct tct gcg tgg acg gtg tcg     3974
Met Ala Gly Pro Gly Ser Pro Ala Ala Ala Ser Ala Trp Thr Val Ser
1165                1170                1175                1180

cct cgt gtg ctc gtg ctc gtg gct ctg tat ccg tgg cac tgt ctc cgt     4022
Pro Arg Val Leu Val Leu Val Ala Leu Tyr Pro Trp His Cys Leu Arg
                1185                1190                1195

ggc act ctg ctc cct tgg ctt gcc tgt ggc cca tag ccccagccct          4068
Gly Thr Leu Leu Pro Trp Leu Ala Cys Gly Pro  *
            1200                1205
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Asn Ile Leu Pro Val Val Glu Arg Cys Met Gly Ala Met Gln Glu Gly
        35                  40                  45
Met Gln Met Val Lys Leu Arg Gly Gly Ser Lys Gly Leu Val Arg Phe
    50                  55                  60
Tyr Tyr Leu Asp Glu His Arg Ser Cys Ile Arg Trp Arg Pro Ser Arg
65                  70                  75                  80
Lys Asn Glu Lys Ala Lys Ile Ser Ile Asp Ser Ile Gln Glu Val Ser
                85                  90                  95
Glu Gly Arg Gln Ser Glu Val Phe Gln Arg Tyr Pro Asp Gly Ser Phe
            100                 105                 110
Asp Pro Asn Cys Cys Phe Ser Ile Tyr His Gly Ser His Arg Glu Ser
        115                 120                 125
Leu Asp Leu Val Ser Thr Ser Ser Glu Val Ala Arg Thr Trp Val Thr
    130                 135                 140
Gly Leu Arg Tyr Leu Met Ala Gly Ile Ser Asp Glu Asp Ser Leu Ala
145                 150                 155                 160
Arg Arg Gln Arg Thr Arg Asp Gln Trp Leu Lys Gln Thr Phe Asp Glu
                165                 170                 175
Ala Asp Lys Asn Gly Asp Gly Ser Leu Ser Ile Gly Glu Val Leu Gln
            180                 185                 190
Leu Leu His Lys Leu Asn Val Asn Leu Pro Arg Gln Arg Val Lys Gln
        195                 200                 205
Met Phe Arg Glu Ala Asp Thr Asp Asp His Gln Gly Thr Leu Gly Phe
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Glu Glu Phe Cys Ala Phe Tyr Lys Met Met Ser Thr Arg Arg Asp Leu
225                 230                 235                 240
Tyr Leu Leu Met Leu Thr Tyr Ser Asn His Lys Asp His Leu Asp Ala
                245                 250                 255
Ala Ser Leu Gln Arg Phe Leu Gln Val Glu Gln Lys Met Ala Gly Val
            260                 265                 270
Thr Leu Glu Ser Cys Gln Asp Ile Ile Glu Gln Phe Glu Pro Cys Pro
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Thr Arg Ser Pro Ala Gly Asp Ile Phe Asn Pro Glu His His His Val
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His Gln Asp Met Thr Gln Pro Leu Ser His Tyr Phe Ile Thr Ser Ser
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            340                 345                 350
Asp Met Tyr Ala Trp Val Leu Gln Ala Gly Cys Arg Cys Val Glu Val
        355                 360                 365
Asp Cys Trp Asp Gly Pro Asp Gly Glu Pro Ile Val His His Gly Tyr
    370                 375                 380
Thr Leu Thr Ser Lys Ile Leu Phe Lys Asp Val Ile Glu Thr Ile Asn
385                 390                 395                 400
Lys Tyr Ala Phe Ile Lys Asn Glu Tyr Pro Val Ile Leu Ser Ile Glu
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Asn His Cys Ser Val Ile Gln Gln Lys Lys Met Ala Gln Tyr Leu Thr
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Asp Ile Leu Gly Asp Lys Leu Asp Leu Ser Ser Val Ser Ser Glu Asp
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Ala Thr Thr Leu Pro Ser Pro Gln Met Leu Lys Gly Lys Ile Leu Val
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Lys Gly Lys Lys Leu Pro Ala Asn Ile Ser Glu Asp Ala Glu Glu Gly
465                 470                 475                 480
Glu Val Ser Asp Glu Asp Ser Ala Asp Glu Ile Asp Asp Asp Cys Lys
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Ala Lys Arg Lys Leu Asp Ser Leu Ile Lys Glu Ser Lys Ile Arg Asp
        515                 520                 525
Cys Glu Asp Pro Asn Asn Phe Ser Val Ser Thr Leu Ser Pro Ser Gly
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Lys Leu Gly Arg Lys Ser Lys Ala Glu Glu Asp Val Glu Ser Gly Glu
545                 550                 555                 560
Asp Ala Gly Ala Ser Arg Arg Asn Gly Arg Leu Val Val Gly Ser Phe
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Ser Arg Arg Lys Lys Lys Gly Ser Lys Leu Lys Lys Ala Ala Ser Val
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Glu Glu Gly Asp Glu Gly Gln Asp Ser Pro Gly Gly Gln Ser Arg Gly
        595                 600                 605
Ala Thr Arg Gln Lys Lys Thr Met Lys Leu Ser Arg Ala Leu Ser Asp
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625                 630                 635                 640
Ala Ala Ser Ser Trp Gln Val Ser Ser Phe Ser Glu Thr Lys Ala His
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Gln Ile Leu Gln Gln Lys Pro Ala Gln Tyr Leu Arg Phe Asn Gln Gln
            660                 665                 670
Gln Leu Ser Arg Ile Tyr Pro Ser Ser Tyr Arg Val Asp Ser Ser Asn
        675                 680                 685
Tyr Asn Pro Gln Pro Phe Trp Asn Ala Gly Cys Gln Met Val Ala Leu
    690                 695                 700
Asn Tyr Gln Ser Glu Gly Arg Met Leu Gln Leu Asn Arg Ala Lys Phe
705                 710                 715                 720
Ser Ala Asn Gly Gly Cys Gly Tyr Val Leu Lys Pro Gly Cys Met Cys
                725                 730                 735
Gln Gly Val Phe Asn Pro Asn Ser Glu Asp Pro Leu Pro Gly Gln Leu
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Lys Lys Gln Leu Val Leu Arg Ile Ile Ser Gly Gln Gln Leu Pro Lys
        755                 760                 765
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Pro Arg Asp Ser Met Leu Gly Asp Arg Gly Glu Ile Ile Asp Pro Phe
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785                 790                 795                 800
Thr Arg Val Val Asp Asp Asn Gly Phe Asn Pro Thr Trp Glu Glu Thr
                805                 810                 815
Leu Val Phe Met Val His Met Pro Glu Ile Ala Leu Val Arg Phe Leu
            820                 825                 830
Val Trp Asp His Asp Pro Ile Gly Arg Asp Phe Ile Gly Gln Arg Thr
        835                 840                 845
Leu Ala Phe Ser Ser Met Met Pro Gly Tyr Arg His Val Tyr Leu Glu
    850                 855                 860
Gly Met Glu Glu Ala Ser Ile Phe Val His Val Ala Val Ser Asp Ile
865                 870                 875                 880
Ser Gly Lys Val Lys Gln Ala Leu Gly Leu Lys Gly Leu Phe Leu Arg
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Gly Pro Lys Pro Gly Ser Leu Asp Ser His Ala Ala Gly Arg Pro Pro
            900                 905                 910
Ala Arg Pro Ser Val Ser Gln Arg Ile Leu Arg Arg Thr Ala Ser Ala
        915                 920                 925
Pro Thr Lys Ser Gln Lys Pro Gly Arg Arg Gly Phe Pro Glu Leu Val
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Leu Gly Thr Arg Asp Thr Gly Ser Lys Gly Val Ala Asp Asp Val Val
945                 950                 955                 960
Pro Pro Gly Pro Gly Pro Ala Pro Glu Ala Pro Ala Gln Glu Gly Pro
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Gly Ser Gly Ser Pro Arg Gly Lys Ala Pro Ala Ala Val Ala Glu Lys
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Ser Pro Val Arg Val Arg Pro Pro Arg Val Leu Asp Gly Pro Gly Pro
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Ala Gly Met Ala Ala Thr Cys Met Lys Cys Val Val Gly Ser Cys Ala
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Gly Val Asn Thr Gly Gly Leu Gln Arg Glu Arg Pro Pro Ser Pro Gly
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Pro Ala Ser Arg Gln Ala Ala Ile Arg Gln Gln Pro Arg Ala Arg Ala
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Asp Ser Leu Gly Ala Pro Cys Cys Gly Leu Asp Pro His Ala Ile Pro
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Gly Arg Ser Arg Glu Ala Pro Lys Gly Pro Gly Ala Trp Arg Gln Gly
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Pro Gly Gly Ser Gly Ser Met Ser Ser Asp Ser Ser Ser Pro Asp Ser
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Pro Gly Ile Pro Glu Arg Ser Pro Arg Trp Pro Glu Gly Ala Cys Arg
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Gln Pro Gly Ala Leu Gln Gly Glu Met Ser Ala Leu Phe Ala Gln Lys
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Leu Glu Glu Ile Arg Ser Lys Ser Pro Met Phe Ser Ala Gly Lys Pro
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Leu Leu Pro Cys Val Val Leu Pro His Ala Pro Gly Met Ala Gly Pro
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Gly Ser Pro Ala Ala Ala Ser Ala Trp Thr Val Ser Pro Arg Val Leu
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<213> Homo sapiens

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<210> 4
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid

<400> 4

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Val Ile Lys Glu Gly Trp Leu Leu Lys Lys Ser Lys Ser Trp Lys Lys
 1               5                  10                  15
Arg Tyr Phe Val Leu Phe Asn Asn Val Leu Leu Tyr Tyr Lys Asp Ser
            20                  25                  30
Lys Lys Lys Pro Lys Gly Ser Ile Pro Leu Ser Gly Cys Gln Val Glu
        35                  40                  45
Lys Pro Asp Lys Asn Cys Phe Glu Ile Arg Thr Asp Arg Thr Leu Leu
    50                  55                  60
Leu Gln Ala Glu Ser Glu Glu Glu Arg Lys Glu Trp Val Lys Ala Ile
65                  70                  75                  80
Gln Ser Ala Ile Arg
                85
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<210> 5
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid

<400> 5

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Glu Leu Lys Glu Ala Phe Lys Glu Phe Asp Lys Asp Gly Asp Gly Lys
 1               5                  10                  15
Ile Ser Phe Glu Glu Phe Lys Ala Ala Leu Lys Lys Leu
            20                  25
```

<210> 6
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid

<400> 6

```
Glu Leu Lys Glu Ala Phe Lys Glu Phe Asp Lys Asp Gly Asp Gly Lys
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```
 1               5                  10                  15
Ile Ser Phe Glu Glu Phe Lys Ala Ala Leu Lys Lys Leu
            20                  25
```

<210> 7
<211> 153
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid

<400> 7

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Asp Met Ser Ile Pro Leu Ser His Tyr Phe Ile Ser Ser Ser His Asn
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Thr Tyr Leu Thr Gly Lys Gln Leu Trp Gly Lys Ser Ser Val Glu Ser
            20                  25                  30
Tyr Arg Gln Gln Leu Asp Ala Gly Cys Arg Cys Val Glu Leu Asp Cys
        35                  40                  45
Trp Asp Gly Lys Pro Asp Asp Glu Pro Ile Ile Tyr His Gly His Thr
    50                  55                  60
Leu Thr Leu Glu Ile Lys Leu Lys Asp Val Leu Glu Ala Ile Lys Asp
65                  70                  75                  80
Phe Ala Phe Lys Pro Thr Ser Pro Tyr Pro Val Ile Leu Ser Leu Glu
                85                  90                  95
Asn His Cys Asn Ser Asp Asp Gln Gln Arg Lys Met Ala Lys Tyr Phe
            100                 105                 110
Lys Glu Ile Phe Gly Asp Met Leu Leu Thr Lys Pro Thr Leu Asp Ser
        115                 120                 125
Leu Thr Thr Glu Pro Gly Leu Pro Leu Pro Ser Leu Lys Asp Leu Arg
    130                 135                 140
Gly Lys Ile Leu Leu Lys Asn Lys Lys
145                 150
```

<210> 8
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid

<400> 8

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Glu Leu Ser Asn Leu Val Asn Tyr Ile Gln Ser Ile Lys Phe Arg Ser
 1               5                  10                  15
Phe Glu Leu Ser Gly Glu Glu Lys Asn Thr Ser Tyr Glu Ile Ser Ser
            20                  25                  30
Phe Ser Glu Arg Lys Val Lys Ala Lys Lys Leu Leu Lys Glu Ser Pro
        35                  40                  45
Val Glu Phe Val Lys Tyr Asn Lys Arg Gln Leu Ser Arg Val Tyr Pro
    50                  55                  60
Lys Gly Thr Arg Val Asp Ser Ser Asn Phe Met Pro Gln Val Phe Trp
65                  70                  75                  80
Asn Ala Gly Cys Gln Met Val Ala Leu Asn Phe Gln Thr Ser Asp Leu
                85                  90                  95
Pro Met Gln Ile Asn Asp Gly Met Phe Glu Tyr Asn Gly Gly Gln Pro
            100                 105                 110
```

Asp Gly Ser Phe Lys Ser Gly Tyr Leu Leu Lys Pro Glu Phe Leu Arg
115 120 125

<210> 9
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid

<400> 9
Leu Thr Val Thr Val Ile Glu Ala Arg Asn Leu Pro Lys Met Asp Lys
1 5 10 15
Val Asn Gly Arg Leu Ser Asp Pro Tyr Val Lys Val Ser Leu Leu Gly
20 25 30
Asp Lys Lys Asp Leu Lys Lys Phe Lys Thr Lys Val Val Lys Lys Thr
35 40 45
Asn Gly Leu Asn Pro Val Trp Asn Glu Glu Thr Phe Val Phe Glu Lys
50 55 60
Val Pro Leu Pro Glu Leu Ala Ser Lys Thr Leu Arg Phe Ala Val Tyr
65 70 75 80
Asp Glu Asp Arg Phe Ser Arg Asp Asp Phe Ile Gly Gln Val Thr
85 90 95

<210> 10
<211> 325
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid

<400> 10
Gln Val Lys Gln Ala Leu Gly Leu Lys Gly Leu Phe Leu Arg Gly Pro
1 5 10 15
Lys Pro Gly Ser Leu Asp Ser His Ala Ala Gly Arg Pro Pro Ala Arg
20 25 30
Pro Ser Val Ser Gln Arg Ile Leu Arg Arg Thr Ala Ser Ala Pro Thr
35 40 45
Lys Ser Gln Lys Pro Gly Arg Arg Gly Phe Pro Glu Leu Val Leu Gly
50 55 60
Thr Arg Asp Thr Gly Ser Lys Gly Val Ala Asp Asp Val Val Pro Pro
65 70 75 80
Gly Pro Gly Pro Ala Pro Glu Ala Pro Ala Gln Glu Gly Pro Gly Ser
85 90 95
Gly Ser Pro Arg Gly Lys Ala Pro Ala Ala Val Ala Glu Lys Ser Pro
100 105 110
Val Arg Val Arg Pro Pro Arg Val Leu Asp Gly Pro Gly Pro Ala Gly
115 120 125
Met Ala Ala Thr Cys Met Lys Cys Val Val Gly Ser Cys Ala Gly Val
130 135 140
Asn Thr Gly Gly Leu Gln Arg Glu Arg Pro Pro Ser Pro Gly Pro Ala
145 150 155 160
Ser Arg Gln Ala Ala Ile Arg Gln Gln Pro Arg Ala Arg Ala Asp Ser
165 170 175
Leu Gly Ala Pro Cys Cys Gly Leu Asp Pro His Ala Ile Pro Gly Arg

```
            180                 185                 190
Ser Arg Glu Ala Pro Lys Gly Pro Gly Ala Trp Arg Gln Gly Pro Gly
        195                 200                 205
Gly Ser Gly Ser Met Ser Ser Asp Ser Ser Ser Pro Asp Ser Pro Gly
    210                 215                 220
Ile Pro Glu Arg Ser Pro Arg Trp Pro Glu Gly Ala Cys Arg Gln Pro
225                 230                 235                 240
Gly Ala Leu Gln Gly Glu Met Ser Ala Leu Phe Ala Gln Lys Leu Glu
                245                 250                 255
Glu Ile Arg Ser Lys Ser Pro Met Phe Ser Ala Gly Lys Pro Leu Leu
            260                 265                 270
Pro Cys Val Val Leu Pro His Ala Pro Gly Met Ala Gly Pro Gly Ser
        275                 280                 285
Pro Ala Ala Ala Ser Ala Trp Thr Val Ser Pro Arg Val Leu Val Leu
    290                 295                 300
Val Ala Leu Tyr Pro Trp His Cys Leu Arg Gly Thr Leu Leu Pro Trp
305                 310                 315                 320
Leu Ala Cys Gly Pro
                325
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<210> 11
<211> 158
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid

<400> 11

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Ser Pro Asp Cys Asn Val Phe Asp Pro Glu His Lys Gln Val His Gln
 1                5                  10                  15
Asp Met Asn Gln Pro Leu Ser His Tyr Phe Ile Asn Ser Ser His Asn
            20                  25                  30
Thr Tyr Leu Thr Gly Asn Gln Leu Ser Ser Gly Glu Ser Ser Val Glu
        35                  40                  45
Met Tyr Arg Gln Ala Leu Leu Lys Gly Cys Arg Cys Ile Glu Leu Asp
    50                  55                  60
Cys Trp Asp Gly Lys Asp Gly Asp Pro Glu Pro Ile Ile Thr His Gly
65                  70                  75                  80
His Thr Met Thr Thr Glu Ile Ser Phe Lys Asp Cys Leu Glu Ala Ile
                85                  90                  95
Lys Glu His Ala Phe Val Thr Ser Glu Tyr Pro Val Ile Leu Ser Leu
            100                 105                 110
Glu Asn His Cys Asp Ser Thr Pro Gln Gln Gln Ala Lys Met Ala Glu
        115                 120                 125
Tyr Cys Lys Glu Val Phe Gly Asp Met Leu Phe Thr Glu Pro Leu Glu
    130                 135                 140
Glu Ser Pro Leu Glu Pro Gly Lys Glu Leu Pro Ser Pro Glu
145                 150                 155
```

<210> 12
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid

<400> 12
Lys Arg Lys Ile Leu Ile Lys Asn Lys Lys Leu Lys Glu His Ser Glu
 1   5   10   15
Glu Lys Glu Ser Glu Glu Lys Lys Thr Asp Glu Glu Thr Glu Ser Glu
            20   25   30
Glu Glu Asp Glu Met Gly Ser Asp Ala
        35   40

<210> 13
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid

<400> 13
Pro Gly Lys Glu Leu Pro Ser Pro Glu Glu Leu Lys Arg Lys Ile Leu
 1   5   10   15
Ile Lys

<210> 14
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid

<400> 14
Cys Leu Gln Phe Met Gln Lys Gly Ser Glu Leu Lys Lys Val Arg Ser
 1   5   10   15
Asn Ser Trp Lys Tyr Asn Arg Tyr Phe Thr Leu Asp Asp Asp Met Gln
            20   25   30
Thr Leu Trp Trp Glu Pro His Trp Phe Ser Lys Lys Asp Ser Glu Lys
        35   40   45
Pro Lys Phe Asp Ile Ser Asp Ile Lys Glu Ile Arg Met Gly Lys Asn
    50   55   60
Thr Glu Thr Phe Arg Asn Asn Gly Lys Glu Phe Gln Ile Gln Glu Pro
65   70   75   80
Glu Asp Cys Cys Phe Ser Ile Ile Phe Gly Glu Asn Tyr Phe His Glu
                85   90   95
Ser Leu Asp Leu Val Ala Asn Ser Ala Asp Val Ala Asn Ile Trp Val
            100   105   110
Ser Gly Leu Arg Tyr Leu Val Asp Tyr Ala Lys His Met Leu Asp Asn
        115   120   125
Tyr Gln Glu Gln Leu Asp Gln Trp Leu Arg Glu Trp Phe Gln Gln Ala
    130   135   140
Asp Arg Asn Lys Asp Ser Arg Met Ser Phe Arg Glu Ala Gln Asn Leu
145   150   155   160
Leu Lys Leu Met Asn Val Gln Met Asp Glu Glu Tyr Ala Phe Ser Ile
                165   170   175
Phe Arg Glu Cys Asp
            180

<210> 15
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid

<400> 15
Phe Asp Glu Phe Asp Thr Asp Gly Asn Gly His Leu Asp Glu Gln Thr
1 5 10 15
Ala Phe Lys Cys Ile Lys His Leu Asn Pro Arg Leu Lys His His Lys
20 25 30
Ile Thr Asn Lys Phe Lys Glu Ile Thr Ile Lys Ser Lys Glu Lys Glu
35 40 45
Arg Thr Lys Ile Thr Lys Glu His Phe Val Asp Leu Tyr Lys Glu Leu
50 55 60
Gly Thr Arg Pro Glu Val Tyr Phe Leu Met Val Gln Tyr Ser Lys Asn
65 70 75 80
Lys Asp Tyr Leu Asp Cys Gln Asp Leu Met Leu Phe Leu Glu Thr Glu
85 90 95
Gln Gly Met Val His Val Thr Glu Asp Asn Cys Leu Asp Ile Ile Glu
100 105 110
Gln Tyr Glu Pro Cys Ser Glu Gly Arg Glu Asn Gly Trp Met Thr Ile
115 120 125
Asp Gly Phe Thr Ser Tyr
130

<210> 16
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid

<400> 16
Phe Ser Ser Leu Val Pro Gly Tyr Arg His Val Tyr Leu Glu Gly Leu
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Thr Glu Ala Ser Ile Phe Val His Ile Thr Ile Asn Glu Ile Tyr Gly
20 25 30
Lys Asn Arg Gln Leu Gln Gly Leu Lys Gly Leu Phe Asn Lys Asn Pro
35 40 45
Arg His Ser Ser Ser Glu Asn Asn Ser His Tyr Val Arg Lys Arg Ser
50 55 60
Ile Gly Asp Arg Ile Leu Arg Arg Thr Ala Ser Ala Pro Ala Lys Gly
65 70 75 80
Arg Lys Lys Ser Lys Met Gly Phe Gln Glu Met Val
85 90

<210> 17
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid

<221> VARIANT
<222> (1)...(51)
<223> Xaa = Any Amino Acid

<400> 17

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Gly Asp Asn Gln Gly His Arg Lys Gly Pro Leu Ile Val Met Cys Asp
            20                  25                  30
Glu Asn Gln Ser Thr Ala Gly Cys Xaa Xaa Asp Glu Leu Ile Val Met
        35                  40                  45
Phe Tyr Trp
    50
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